Amendments to the Specification:

Please amend the specification as follows:

Please delete paragraph [0001] and replace it with the following paragraph:

[0001] This application is a continuation-in-part of U.S. application serial number 10/369,324 filed on February 20, 2003, and claims priority to U.S. provisional application serial numbers 60/357,661 filed on February 20, 2002 and 60/377,602 filed on May 6, 2002, which applications are all incorporated herein by reference.

Please delete paragraph [0047] and replace it with the following paragraph:

[0047] In an even more preferred embodiment, the P-DNAs are isolated from any plant by using degenerate primers in a polymerase chain reaction. In one preferred embodiment, the P-DNA is derived from potato, is delineated by 25-bp termini with 80 and 88% identity to conventional T-DNA borders, respectively, and has the nucleotide sequence shown in SEQ ID NO. 1 of SEQ ID NO. 98. In another most preferred embodiment, the P-DNA is derived from wheat, is delineated by 25-bp termini with 72% and 92% identity with conventional T-DNA borders, respectively, and contains the nucleotide sequence shown in SEQ ID NO. 94 or 95 [[34]].

Please substitute Table 10 with the following:

Table 10. PPO activity in potato lines expressing a modified PPO gene

Line	Change in OD-410/gram			
	micro tubers (%-reduced)	mini tubers (%-reduced)	9-week tubers (%-reduced)	12-week tubers (%-reduced)
Untransformed controls	24.59 ± 2.22	20.07 ± 1.21	21.0 ± 3.3	21.0 ± 2.7
Vector controls	22.59 ± 3.36	19.55 ± 1.43	20.6 ± 2.1	22.5 ± 2.2
314-1	2.36 (90%)	17.8 (11%)	19.2 (12%)	22.0 (-9%)
314-2	41.52 (-76%)	21.3 (-7%)		
314-4	18.40 (22%)	5.4 (73%)	19.0 (13%)	16.7 (17%)
314-5	8.49 (64%)	19.1 (4%)	24.2 (-11%)	26.8 (-33%)
314-7	16.04 (32%)	16 (20%)		
314-8	14.86 (37%)	17 (15%)		
314-9	5.43 (77%)	4.3 (78%)	3.7 (83%)	2.8 (86%)

314-12	19.35 (18%)	19.6 (2%)		
314-13	18.17 (23%)	15.4 (23%)		
314-14	18.64 (21%)	17.32 (13%)		
314-16	13.92 (41%)	18.2 (9%)		
314-17	5.19 (78%)	2.4 (88%)	4.8 (78%)	1.2 (94%)
314-20	26.66 (-13%)	13.2 (34%)	29.2 (-34%)	18.2 (10%)
314-21	11.32 (52%)	17.6 (12%)		
314-22	13.45 (43%)	18.8 (6%)		
314-23	5.19 (78%)	20.4 (-2%)	19.9 (8%)	15.8 (22%)
314-24	15.10 (36%)	19.6 (2%)		
314-25	23.12 (2%)	19 (5%)		
314-26	13.45 (43%)	17.8 (11%)		
314-27	26.42 (-12%)	19.4 (3%)		
314-28	31.85 (-35%)	19.4 (3%)		
314-29	3.77 (84%)	14.8 (26%)	22.1 (-2%)	18.3 (9%)
314-31	23.83 (-1%)	21.2 (-6%)		
314-32	28.78 (-22%)	20 (0%)		

Please substitute Table 11 with the following:

Table 11. PPO activity in potato minitubers expressing a modified trailer sequence associated with the PPO gene

Line	Change in OD-410/gram (%-reduced)		
	mini tubers	9-week tubers	12-week tubers
Untransformed controls	20.6 ± 1.3	21.0 ± 3.3	
Vector controls	17.9 ± 2.1	20.6 ± 2.1	
217-1	12.5 (39.4%)		
217-4	12.6 (38.6%)		
217-5	11.3 (45.0%)		
217-6	6.1 (70.4%)	4.72 (78%)	2.44 (88%)
217-7	5.7 (72.5%)	3.68 (83%)	1.92 (90%)
217-9	10.4 (49.6%)		
217-10	15.2 (26.3%)		
217-11	15.2 (26.3%)		
217-12	6.6 (67.9%)	4.24 (80%)	2.84 (86%)
217-14	15.4 (25.4%)		
217-15	13.5 (34.6%)		
217-16	6.0 (71.0%)	2.12 (90%)	2.84 (86%)
217-17	9.7 (53.0%)		
217-19	8.6 (58.4%)	4.60 (79%)	3.2 (84%)
217-21	14.2 (31.1%)		
217-22	9.7 (53.0%)	2.56 (88%)	4.8 (76%)
217-23	15.2 (26.3%)		
217-24	8.2 (60.1%)		3.24 (84%)
217-25	11.9 (42.2%)		
217-26	3.1 (84.8%)	2.20 (90%)	2.32 (89%)
217-27	6.2 (69.9%)	10.28 (53%)	6.08 (70%)
217-29	7.2 (65.1%)	5.04 (77%)	3.92 (81%)

Please delete paragraph [0215] and replace it with the following paragraph:

[0215] The border-like sequences of the present invention can be isolated from any plant, such as from potato and wheat. See SEQ ID NOs. 1 and 98 and SEQ ID NO. 34, for sequences which contain, at either end, the border-like sequences isolated from potato ~~and wheat respectively~~. Thus, a P-DNA left and right border sequences of use for the present invention are isolated from and/or native to the genome of a plant that is to be modified. A P-DNA border-like sequence is not identical in nucleotide sequence to any known *Agrobacterium*-derived T-DNA border sequence.. Thus, a P-DNA border-like sequence may possess 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more nucleotides that are different from a T-DNA border sequence from an *Agrobacterium* species, such as *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*. That is, a P-DNA border, or a border-like sequence of the present invention has at least 95%, at least 90%, at least 80%, at least 75%, at least 70%, at least 60% or at least 50% sequence identity with a T-DNA border sequence from an *Agrobacterium* species, such as *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*, but not 100% sequence identity. As used herein, the descriptive terms "P-DNA border" and "P-DNA border-like" are exchangeable.

Please delete paragraph [0120] and replace it with the following:

[0120] In yet another embodiment, the isolated nucleotide sequence is isolated from potato, and has a nucleotide sequence shown in either SEQ ID NOs. ~~94 or 95~~ 1, 54, 55 or 98. In a preferred embodiment, the isolated nucleotide sequence shares 52% sequence identity with a T-DNA border sequence from Agrobacterium tumafaciens. The present invention encompasses a vector that comprises such nucleotide sequences.

On page 129, line 1, after the words "into the" delete the word [[toxic]]. Hence, please delete paragraph [0391] and replace it with the following:

[0391] The previous example demonstrates that the efficiency of marker-free transformation is several-fold lower with a modified P-DNA than with a conventional T-DNA. To improve the efficiency of generating shoots only containing a modified P-DNA, an expression cassette for a suicide gene fusion comprising the bacterial cytosine deaminase

(*codA*) and uracil phosphoribosyltransferase (*upp*) genes (InvivoGen, CA) was inserted between T-DNA borders of the LifeSupport vector, generating pSIM346 (Figure 5). Potato stem explants were infected with one strain carrying pSIM340 and the other carrying pSIM346, and subsequently placed on the following media: (1) co-cultivation media for 2 days, (2) CIMTK media to select for transient marker gene expression for 5 days, (3) CIMT media to allow proliferation of plant cells that transiently expressed the marker gene for 30 days, (4) SIMT media with 500 mg/L of non-toxic 5-fluorocytosine (5-FC), which will be converted by plant cells expressing *codA::upp* into the [[toxic]] toxic 5-fluorouracil (5-FU), to select against stable integration of the LifeSupport TDNA. Callus gave rise to shoots on SIMT within 4 weeks. These shoots were transferred to MS media with timentin and allowed to grow until sufficient tissue was available for PCR analysis. DNA was then extracted from 100 shoots and used to determine the presence of P-DNA, LifeSupport and backbone. As shown in Table 15, none of the shoots analyzed contained a LifeSupport T-DNA, indicating, for the first time, that the *codA::upp* gene fusion can be used as negative selectable marker prior to regeneration. More importantly, these results demonstrate that a negative selection against LifeSupport T-DNA integration increases the frequency of shoots that only contain a modified P-DNA. By coupling a positive selection for transient marker gene expression with a negative selection against stable integration of the *codA::upp* gene fusion, the frequency of shoots only containing a modified P-DNA is about 5-fold higher than by only employing the positive selection for transient marker gene expression (Table 15).